

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 23:36:15 ; Search time 5307.2 Seconds
(without alignments)
2746.592 Million cell updates/sec

Title: US-09-719-748-1_COPY_62_1141
Perfect score: 1080
Sequence: 1 atgagacatcaacagcagca.....ggagagagagacagcactcc 1080

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	781	72.3	1729	11	AK004350	AK004350 Mus muscu
2	604.2	45.3	882	9	AI322362	AI322362 me98c10.y
3	532.6	49.3	830	10	BG68701	BG68701 602787522
4	512.8	47.5	976	11	BC012210	BC012210 Mus muscu
5	506.6	46.9	1199	11	AK009701	AK009701 Mus muscu
6	506.4	46.9	940	10	BE883503	BE883503 601511064
7	499.2	46.2	972	10	BT554559	BT554559 603235693
8	495.6	45.9	649	10	BT046467	BT046467 MR3-FN020
9	486.8	45.1	555	10	BF087508	BF087508 QV2-HT054
10	459.2	42.5	869	10	W82116	W82116 me98c10.r1
11	453.4	42.0	585	10	BG384579	BG384579 303638 MA
12	434.6	40.2	565	10	BF075625	BF075625 224820 MA
13	431.6	40.0	999	10	BF168866	BF168866 60175325
14	429.8	39.8	1127	10	BF733365	BF733365 601567911
15	428.2	39.6	671	10	BF727181	BF727181 by17h06.y
16	425.6	39.4	556	10	BF075639	BF075639 224840 MA
17	425.6	39.4	982	10	BF976537	BF976537 602244391

18	415.4	38.5	708	9	AM476323	AM476323 uq3f11.y
19	411.2	38.1	696	10	BF012103	BF012103 ux53g01.y
20	409	37.9	1058	10	BG421064	BG421064 602451186
21	408.4	37.8	460	9	AA858002	AA858002 o163g08.s
22	408.2	37.8	663	10	BF019568	BF019568 ux12f12.y
23	402.8	37.3	681	10	BF149425	BF149425 602848986
24	402	37.2	481	9	AM603538	AM603538 RCO-CN002
25	402	37.2	887	10	BF6968191	BF6968191 602835674
26	397.8	36.8	871	10	BF690902	BF690902 603312045
27	397.4	36.8	855	10	BF128782	BF128782 603074924
28	394.2	36.5	703	10	BG685492	BG685492 602783624
29	393	36.4	756	10	BF162798	BF162798 601769262
30	388.8	36.0	796	10	BG421646	BG421646 602449739
31	386.8	35.8	797	10	BF163166	BF163166 603286787
32	380.6	35.2	710	10	BG277312	BG277312 ux42b06.y
33	377	34.9	1039	10	BG419640	BG419640 602451855
34	375.6	34.8	785	10	BF152999	BF152999 603299971
35	374.2	34.6	707	10	BF1904738	BF1904738 603168651
36	371.4	34.4	654	10	BF012312	BF012312 BF012312
37	370.6	34.3	441	9	AA718515	AA718515 VR84F03.F
38	369	34.2	798	10	BG682263	BG682263 602795580
39	364.2	33.7	693	9	AL631486	AL631486 AL631486
40	355.6	32.9	743	10	BG368192	BG368192 6028356
41	355.4	32.9	958	10	BF157256	BF157256 603030761
42	354.6	32.8	623	10	BE848999	BE848999 uw01907.y
43	354.4	32.8	622	10	BF1414743	BF1414743 602991133
44	352.2	32.7	433	10	W34247	W34247 mb80c12.r1
45	352.2	32.6	548	10	BF558103	BF558103 UT-R-C0-h

ALIGNMENTS

RESULT	1	1729 bp	muscle	linear	HTC 19-JAN-2002
AK004350	AK004350	1729 bp	muscle	linear	HTC 19-JAN-2002
LOCUS	AK004350	1729 bp	muscle	linear	HTC 19-JAN-2002
DEFINITION	AK004350	1729 bp	muscle	linear	HTC 19-JAN-2002
ACCESSION	AK004350	1729 bp	muscle	linear	HTC 19-JAN-2002
VERSION	AK004350.1	1729 bp	muscle	linear	HTC 19-JAN-2002
KEYWORDS	HTC; CAP trapper.	1729 bp	muscle	linear	HTC 19-JAN-2002
SOURCE	Mus musculus (Strain: C57BL/6J) 18 days embryo cDNA to mRNA, clone lib: RIKEN full-length enriched mouse cDNA library clone: 1110062102.	1729 bp	muscle	linear	HTC 19-JAN-2002
ORGANISM	Mus musculus	1729 bp	muscle	linear	HTC 19-JAN-2002
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1729 bp	muscle	linear	HTC 19-JAN-2002
AUTHORS	1 (sites)	1729 bp	muscle	linear	HTC 19-JAN-2002
TITLE	Carninci, P. and Hayashizaki, Y.	1729 bp	muscle	linear	HTC 19-JAN-2002
JOURNAL	High-efficiency full-length cDNA cloning	1729 bp	muscle	linear	HTC 19-JAN-2002
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)	1729 bp	muscle	linear	HTC 19-JAN-2002
PUBMED	99279253	1729 bp	muscle	linear	HTC 19-JAN-2002
REFERENCE	10349636	1729 bp	muscle	linear	HTC 19-JAN-2002
AUTHORS	2 (sites)	1729 bp	muscle	linear	HTC 19-JAN-2002
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	1729 bp	muscle	linear	HTC 19-JAN-2002
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	1729 bp	muscle	linear	HTC 19-JAN-2002
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)	1729 bp	muscle	linear	HTC 19-JAN-2002
PUBMED	20499374	1729 bp	muscle	linear	HTC 19-JAN-2002
REFERENCE	3 (sites)	1729 bp	muscle	linear	HTC 19-JAN-2002
AUTHORS	Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itch, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	1729 bp	muscle	linear	HTC 19-JAN-2002
TITLE	RIKEN Integrated sequence analysis (RISA) system-384 format	1729 bp	muscle	linear	HTC 19-JAN-2002
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	1729 bp	muscle	linear	HTC 19-JAN-2002

RESULT 2
 AI322362 882 bp mRNA linear EST 23-DEC-1998
 LOCUS image10.y1 Soares mouse p3NMFL9.5 Mus musculus cDNA clone
 DEFINITION IMAGE:03602.5 similar to gb:01496 Mouse MHC, class III antigen,
 factor B (MOUSE); mRNA sequence.
 ACCESSION AI322362.1 GI:4056791
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 882)
 AUTHORs Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Schelberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:247370
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq primer: 40RP from Gibco
 High quality sequence stop: 442.
 Location/Qualifiers
 1..882
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:403602"
 /clone_11b="Soares mouse p3NMFL9.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="vector: pT73D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5,
 TGTTCACATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'],
 TGTTCACATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 BASE COUNT 246 a 210 c 227 g 193 t 6 others
 ORIGIN
 Query Match 55.9%; Score 604.2; DB 9; Length 882;
 Best Local Similarity 87.7%; Pred. No. 4.3e-129;
 Matches 690; Conservative 0; Mismatches 94; Indels 3; Gaps 3;
 Oy 170 gccggagagagatcgagcgagggtgagcatctcgcgcaggtctgcacacacatgtca 229
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 GCCGGAGGAAATCGAGCGGAGGTAGCATCTCGCGGAGGTGCTGCACCCACATCA 60
 Oy 230 tcaacgtgcacagcgtctatgaaacgcacgcagctgtgtgcacatccttgagctgtgt 269
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 TCACGAGGACGACGCTTATGAGAACCGCACGACGTGGGTCTATCCTTGACCTAGTGT 120
 Oy 290 ctgagagagagctcttcgattcttcgcccagagagagctacgtgagtgagagagcaca 349
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 CCGAGAGAGAACTGTTTATTCCTCGCCCGAGAGAGTCGTTAAGTAGAGAGAAACCA 180
 Oy 350 ccaagctcatgaagcaatctcgtatgagtgagtaactccttcacacaagaatgtctc 409
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 CGAGCTTCATTAAGCAATCTCGATGGGTGATTTACCTTCACACAAAGAAATTCCTC 240
 Oy 410 acttgatcacaagcccaaaacatlatgttgttagacaagaatlatccatccacaca 469
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 ACTTTGATCTCAAGCCAGCAAAACATCATGTTGTAGACAGAAATATCCCAATTCACACA 300
 Oy 470 tcaagctgattgacttgtgtcgtcgaagaatagaagaatgagtgaaatlaagaata 529
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 TCAAGCTGATTGACTTTGGCTGCTCCGCAAAATAGAAAGATGGAGTTGAATTTAAAAACA 360
 Oy 530 ttcttgagagccggaatttgtgtcgcagaatltgtaactcgaagccctgtgtctg 589
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 TTTTGGGACACCTGGAATTTGTGCTCAAAATCGAAACTATGACCCTGAGCTGG 420
 Oy 590 agcctgacatgtgagatagagcgtcatcacctacatcctcttaagtgtgacatccctt 649
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 AGGCCGACATGTGAGAGCATTTGAGATCATCACTATATCTTCTTAGTGAGAGCTGCC -C 479
 Oy 650 tcttgtagacacagaaagcaagaaacactgtgcaaatatcacatcagtgagtgacttg 709
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 480 TCCTGGGAGACAGACAGAAACCAAGAAACCTGCTATATACCTGCTGTGATGACACTNTG 539
 Oy 710 atgagatctcttcagcatagagcagagctgtgccaagagcttatcgcgaagctctg 769
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 Db 540 ATGAGGATCTTCAGCCAGACAGAGAGCTGGCCAAAGACTTATTCGNAAGCTCTTG 599
 Oy 770 ttaaagagaccggaagacggtcacaatccaagagctcacaagaccctgtgacagc 829
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 Db 600 TGANAGAGACCCGGANNGGCTTACATCCAAAGAGCTTCAGACATCTCTGATACAGC 659
 Oy 830 cggltgacaacccagcaagcgaatgtgagcagggagtgctgtcaatcgtgagaactca 889
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 Db 660 CCGTGACACCCAGCAAGATTTGTACGACAGAGTTCGTGTCACCACTGAGAAATTTTA 719
 Oy 890 ggaagcagatgtcgcgagcggtgtgagagcttccctcagcatcgtgtccctgtgacac 949
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 Db 720 GAAAGCAG-ATGTTCCAGAACCGGGGAAAGCTTGNCCTTACATCGCTCTTG-GCAACC 777
 Oy 950 acctcac 956
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 778 ACCTAAC 784
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
 BG868701 830 bp mRNA linear EST 28-MAY-2002
 LOCUS 602787522F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4913788 5
 DEFINITION mRNA sequence.
 ACCESSION BG868701
 VERSION BG868701.1 GI:14219241
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 830)
 AUTHORs NIH-MGC http://mgc.nci.nih.gov/
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLAM10819 row: k column: 05

High quality sequence stop: 826.
Location/Qualifiers
1. .830
/organism="Mus musculus"
/strain="FVB/N"
/db.xref="taxon:10090"
/clone="IMAGE:4913788"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pcwv-sport6; Site: 1;
Not: Site 2: Sal: Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 217 a 205 c 244 g 163 t 1 others
ORIGIN

Query Match 49.3%; Score 532.6; DB 10; Length 830;
Best Local Similarity 90.6%; Pred. No. 1.4e-112;
Matches 623; Conservative 0; Mismatches 60; Indels 5; Gaps 5;

QY 1 atggagccatcaagcagaagtgtaggagctttagacatcgagagagctgggg 60
DB 143 ATGAGAGAGCTTCAAAACAGCAGAGGTGAGACTTTATGACATCGAGAGAGCTGGGC 202

QY 61 agtggccagttgccatcgtgaagaagtgcgggagaagaacggggcttgatgca 120
DB 203 AGTGGCCAGTTGGCATCTGTAAGAGAGTCCGGGAGAGACACAGGCTGAGATGCA 262

QY 121 gccaaattcatcaagaagcagagccgggcggagccgggtgtgagccggagagag 180
DB 263 GCCAAGTTTCATTAGAGAGAGCAGAGCCGGCCAGCCCTCGGGCGTTCGGGAGAGA 322

QY 181 atcgaagcggaggtgagatcctgcggcagggtgcgcacacaaatgcatcagctgac 240
DB 323 ATCAGAGCGGAGGTGAGCATCTCGGGCAGGTGCTGACACCCACATCATCAGCTGCAC 382

QY 241 gaagctatgagaacccgacgagctggtgacatccttgagctgagtgctggagagag 300
DB 383 GACGTCTATGAGAACCCAGACGAGCTGCTCATCTTGAAGTATGTCGGAGAGAGA 442

QY 301 cctctcgaattccctggcccaagaagagctgagtgagagggagccacagctcat 360
DB 443 CTGTTTGAATTCCTGGCCCAAGAGAGTCCTTAAGTGAAGAGAGAGCCACCACTTCATT 502

QY 361 aagcagatcctggaatggggtgaactaccctcacacaagaagaatgtcactatgctc 420
DB 503 AAGCAGATCCTGATGGGTGAATTACCTTCACACAAAGAAATGGCTCAGCTTGATCTC 562

QY 421 aagcagaagaacattatgtgtta-gacaagaatatatccatccacacatcaagctat 479
DB 563 AAGCCAGAAACATCATGTTGTTAGCAGACAAATATCCCATTCACATCAAGCTGAT 622

QY 480 tgaatttgctgctcaagaaatagaagatgga-gtgaatttaagatatc-cttggg 537
DB 623 TGATTTGGCTGCTCAGCAAAATAGAAGATGAGCTTGATTTAAACATTTGTTTGGG 682

QY 538 acgcgggaattgtgtcctcaagaatgtgaactaagacccctggg-tctggagagctga 596
DB 683 ACACCTCAATTTGTTGCTCCAGAAATCGTGAATATGAGCCACCTGGGAAGTGGCA 742

QY 597 catgtgagatagaggtcaatcacctacatcctcttaagttagagacatcccttccctgg 656
DB 743 CATGTGAGCATTTGGAGTCATCACCTTAATCTTTCTAGTGGAGCGTCCCT-TTCTTGGG 801

QY 657 agacaggaagcagaagaacactggaat 684
DB 802 AGACACAACAGAAACCTTGCAAAATT 829

RESULT 4
BC012210 976 bp mRNA 1linear HTC 08-AUG-2001
LOCUS BC012210 976 bp mRNA 1linear HTC 08-AUG-2001

DEFINITION Mus musculus, Similar to Death-associated like kinase, clone
IMAGE:3993055, mRNA.
ACCESSION BC012210
VERSION BC012210.1 GI:15126556
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 976)
REFERENCE Strausberg R.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.R., Luna, R.A., Hale, S.M., Huiyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Munry, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL, at: http://image.lnl.gov
Series: IRAC Plate: 23 Row: n Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomscan gene
prediction, similarity but not identity to protein
This clone has the following problem: Incomplete processing.
Location/Qualifiers
1. .976
/organism="Mus musculus"
/db.xref="taxon:10090"
/clone="IMAGE:3993055"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
old, gross tissue."
/clone_id="NCI_CGAP_Man5"
/lab_host="DH10B"
/note="Vector: pcwv-sport6"
BASE COUNT 240 a 271 c 294 g 171 t
ORIGIN

Query Match 47.5%; Score 512.8; DB 11; Length 976;
Best Local Similarity 76.2%; Pred. No. 5.7e-108;
Matches 631; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1 atggagccatcaagcagaagtgtaggagctttagacatcgagagagctgggg 60
DB 95 ATGTCCACATTCAGCAGAGAGATGTTGAGACCAATTATGAGATGGAGAGAGCTTGGC 154

QY 61 agtggccagttgccatcgtgaagaagtgcgggagaagaagcggggcttgaatgga 120
DB 155 AGTGGCAATTTGGCATGCTGGCAGAGTCCAGCAAGAGGCAAGGCGCATGGAATGGA 214

QY 121 gccaaattcatcaagaagcagagccgggcggagccggcggtgtgagccggagagag 180
DB 215 GCCAAGTTTCATTAGAGAGCGGCGCTGCCATCCACCGCGGCTGTGACCGGAGAGAG 274

QY 181 atcgaagcggaggtgagatcctgcggcagggtgcgcacacaaatgcatcagctgac 240
DB 275 ATCGAAGCGAGGTGAGCATCTCGGGCAGAGATCCGACCCACACATCATTAACATGCA 334

QY 241 gaagctatgagaacccgacgagctggtgcacatccttgagctagtgctcgagagagag 300

[illegible]

TITLE	Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL	RIKEN Integrated sequence analysis (RISA) system--384-format
PUBLISHED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	20530913
AUTHORS	4 (sites) 11076681
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
PUBLISHED	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 1199)
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bonio, H., Brownstein, M., Bult, C., Cardinaci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirooka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, S., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schiraldi, L., Shidata, K., Shidata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yananaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-Jul-2000)
PUBLISHED	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
REFERENCE	
AUTHORS	Please visit our web site (http://genome-gsc.riken.go.jp/) for further details.
TITLE	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATTCGAGTTAATTAATTAATGATCCCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rct = 5.0 and subtraction to Rct = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATGATCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.
TITLE	Location/Qualifiers
JOURNAL	1. .1199
PUBLISHED	/organism="Mus musculus"
REFERENCE	/strain="C57BL/6J"
AUTHORS	/db_xref="MGD:GI:1901785"
TITLE	/db_xref="taxon:10090"
JOURNAL	/clone="2310039H24"
PUBLISHED	/sex="male"
REFERENCE	/tissue_type="tongue"
AUTHORS	/clone_lib="RIKEN full-length enriched mouse cDNA library"
TITLE	/dev_stage="adult"
JOURNAL	165. >1199
PUBLISHED	/note="DEATH ASSOCIATED PROTEIN KINASE
REFERENCE	data source:SEPR, source key:09Jup7, evidence:ISS
AUTHORS	putative"
TITLE	/codon_start=1
JOURNAL	/protein_id="BAB26448.1"
PUBLISHED	/db_xref="GI:12844658"
REFERENCE	/translation="MTVFRQDNVDYDTGEEAGSGPFAVVKCRKSTGLQVAKTIT
AUTHORS	KRRKTKSSRGVREDIEREISLKEIRHPVITLHEVEYENKTDVILILEVAGGELEF

DFLAEKESLITEEATEFLKQILSGVYLHSIQIAHFIDKBNIMLDRNPKPRIKII
 DFGIAHKIDRGENEKNIFGTEPEVAPEIVNEPEGLADMSISIVITYIILSGASPL
 GDFKQETLDVANSVNDGEEFEENFTSLAKDFRRLVDPKRTMIOJSLQHPWIK
 PKDQOALSRRKASAVNNNEKFRFARAKKNVRLCGHIEFECFLVSEPHSSNNGNE
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 1182..1187
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 1199
 polyA_site
 /note="putative"
 1199
 BASE COUNT 330 a 271 c 342 g 256 t
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 Query Match 46.9%; Score 506.6; DB 11; Length 1199;
 Best Local Similarity 71.9%; Pred. No. 1.7e-106;
 Matches 662; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

10 ttcaagcagcgaaggtgtaggactttatgacatcgagagagctgggaggtgagcag 69
 174 TTCAGCGAGAAACGTGACGACTACTACGACACCGCGGAGGAACTGGCGAGTGGACAG 233
 70 ttgcacatgtagaaggtgcgagagagagacagcggtgtagatgacagccagttc 129
 224 TTGCGAGTTGAGAGAAATGTCGTAGAAAAGTACCGGCTTTCATATGCGCCCAAGTTC 293
 130 atcaagacgagcagagcgcgagcgagcggtgtagcgagagagagatcgagcg 189
 294 ATCAAGAAAGAGAGACCAAGTCACGCGCGGCGGTGACGCGGAGAGACATCGAGCGG 353
 190 gagtgagacatctgtagcaggtgtagcagcagatgtagcagctgtagcagagctat 249
 354 GAGGTGACATCTCTGAAGAGATCCGACCCAAATGTCATCACCCTCATGAGGTCTAT 413
 250 gagaacccagcagcagctgtagcagcagcagcagcagcagcagcagcagcagc 309
 414 GAGAACAGACAGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 473
 310 ttctgtgcccagagagtagttagttagttagttagttagttagttagttagttagt 369
 474 TTCTGTGCTGAGAGAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 533
 370 ctgtagtggtgtagaactctcagcagaaatgtagcagcagcagcagcagcagcag 429
 534 CTCAGCGCGGTTTACTACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACT 593
 430 aacatgattgttagaagaataatccatccacacacacacacacacacacacacacac 489
 594 AACATATGCTTCTGATAGAAATGTCGCAAAACCTCGGATCAAGATCATAGACTTTGGC 653
 490 ctggtcagcagaatagagtagttagttagttagttagttagttagttagttagttagt 549
 654 TTGCGCCCAATAAATGACTTTGGAATGATCAAAACATATTTGGGACACCAAGATT 713
 550 gttgtcagcagaatgtagaactagcagcagcagcagcagcagcagcagcagcagcag 609
 714 GTGCTGTCGGAGATAGTCAACTATAGCCCTGGGTCTTGAAGGCGAGATATGAGGACATC 773
 610 ggcgtcag 669
 774 GGGGTAAATACCTATATCTCTCTAGTGGGCGCTCCCTTTCTTGGAGACACCAAGCAA 833
 670 gaaacacgtgcaaatatcacatcagtgtagcagcagcagcagcagcagcagcagcag 729
 834 GAACATTTAGCGAATGTGCGCGCTGTCAACTACGACTTTGAAGAGAAATTTCTTCGGAAC 893
 730 acgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 789
 894 ACCATACCTCTGCGAAAGATTTCATCAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 953
 790 ctcaaatccaaagaggtctcagacacccctgtagcagcagcagcagcagcagcagcagc 849
 954 ATGACAAATCCAGACAGTGTTCAGACACCCCTGATCAAGCCTTAAGACACCAACACAGCA 1013

850 atgtgcagcggaggtctgtgtagcagcagcagcagcagcagcagcagcagcagcag 909
 1014 CTTACTCGAAGAGCCTCAGCAGTAATGAGAAATTCAGAGAGGTTTCCAGCTCGAANA 1073
 910 cgtgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 930
 1074 AATGGAAGTAAAGACTCTGC 1094
 RESULT 6
 BE883503
 LOCUS
 DEFINITION
 601511064F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912806 5',
 mRNA sequence.
 BE883503
 ACCESSION
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 940)
 NIH-MGC http://mhc.nci.nih.gov/.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 CONTACT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 TISSUE
 Tissue Procurement: ATCC
 CDNA LIBRARY
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA SEQUENCING
 DNA Sequencing by: Inyte Genomics, Inc.
 CLONE DISTRIBUTION
 MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 PLATE
 Plate: LLM9731 row: 0 column: 15
 High quality sequence stop: 643.
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 /db_xref="taxon:9606"
 /clone="IMAGE:3912806"
 /clone_lib="NIH-MGC_71"
 /tissue_type="telomerosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: PCMV-SpOrf6; Site: 1; NCI;
 Site: 2; Salt; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb.
 BASE COUNT 224 a 263 c 280 g 173 t
 ORIGIN
 Query Match 46.9%; Score 506.4; DB 10; Length 940;
 Best Local Similarity 98.5%; Pred. No. 1.7e-106;
 Matches 532; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

535 ggaagcgcggaattgtgtctccagaatgtgtagaactagcagcagcagcagcagcagc 594
 1 GCGAGCGCGGAATTTGCTGCTCCAGAAATGGAATGAGACGCCCTCGGCTGAGGCT 60
 595 gacatgtgtagatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 654
 61 GACATGTGAGCATAGGCTCATACCTACATCTCTTAAAGTGGAGCATCCCTTTCCAG 120
 655 gagaacacgaagcagaac 714
 121 GGAGACACGAACAGGAACAACAGTGAATATACAGCAGAGTGTAGACTTTGATGAG 180
 715 gaattctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 774
 181 GAATCTTCAGCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
 775 gagacccggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 834

QY	128	tcataaagaacgagagacccggcgagccggcgagcgtgtgtgaagccggagagaaatcgaac	187
Db	123	TCATCAAGAAGGGGCGCTGCATCAGCCGGCGGGGTGAGCGGGAGAGATCGAAC	182
QY	188	ggagagtgagcatctctgcgaggtgtgtgtcacaacaatgtcatcagctgaagcgtct	247
Db	183	GGAGGTGAGCATCTGTGGCGAGATCCGCCACCCCMATCATTAACCTGCATCAGCTGT	242
QY	248	atgaagaacgcagccagctgtgtgacatcccttgagctagtgtctggaggaagctcttcg	307
Db	243	TCGAAGAACAAGACMATGTGGTGTGATCTTGAGAGAGTGTGTCCGGTGGCAAGCTTTTCG	302
QY	308	attctctggcccaagaagaagtcacttgaatgaaggaggaagccaccagcttcataagcaga	367
Db	303	ACTTCTCTGGCGGAGAGAGAGTCAATTGACGGAGAGATGAGAGCCACGACGATCTCTCAACAAA	362
QY	368	tccttgatgtgggtgaaactacatcacaagaagaatgtcacttgaatctcgaagccag	427
Db	363	TCTGTAGACGGTGTCCACTACCTGCACCTCAAGCGCATGCGACATTTGACCTGGAAGCCCG	422
QY	428	aaaataatgttgttgaacagaatattcccatctcacaataaagcttgttaacttg	487
Db	423	AGAAATATATGTGTGTGAGACAAGCACGACGACGACCCCGCATTTAAGCTCATCAACTTTG	482
QY	488	gtctgtgtccagaagaatagaatgtgaatgaatgaatatttttggagccggagat	547
Db	483	GCATCGCGCCACAGATGCAAGGCTGGCAGCCAGATTCAGAAATCTTTTGGCACACCCAGT	542
QY	548	ttgtgtgtccagaagaatgtgaactaagagcccttggtgtcgtgagagctgaatgtgagca	607
Db	543	TTGTGTGCCCCCGAGATCGTGAATATGAGCCACTTGTGCTTGAGAGCTGACATGTGGAGCA	602
QY	608	tagcggtatataccataactctcttaagtgaagatcccccttctctgtggagaaacgaagc	667
Db	603	TTGGGTATATCACTACCTACCTCTCTGACGGAGGCTCCCAATTCCTGGGCAAGCAAGC	662
QY	668	aggaacacctgtgcaaatatcacaatgaatgaatgaatgaatgaatgaatgaatgaatgaat	727
Db	663	AGGAGACGCTGACGAACTCTCAGCAGTGAAGTGAATTTGATGAGAGAAATACCTTCAGCA	722
QY	728	atacagcagcagctgtgcaagaacttattcggaaagctctgtgttaagaagaccggaaac	787
Db	723	GCACCGAGAGCTGGCCCAAGGACTTCATCCGAGGCTGTGTCAAGAACCCCAAGAGGA	782
QY	788	ggct 791	
Db	783	GGAT 786	

Db 325 GAGCTTTGAGAACGACGACGCTGCTCATCTCTGAGCTAGTGTGTGAGAGAG 384
Oy 301 cctctgattccttgccaggaagaagtaactgagtgaggaaggaccagcttcatt 360
Db 385 CTCCTTGACTTCTGCGCCAGAGAGAGTCCCTGAGTGAGAGAGAGCGACCACTTCATT 444
Oy 361 aagcagaatcctgagtgagggtgaaactccttcacacaaagaagaatttcactgagtc 420
Db 445 AACGACATCTCGATGGGGGAGAACTCACTTCAGCCAAAGAAATTCCTCACTTGATCTC 504
Oy 421 aagcagaagaacatactgctgttagaagaagaatattccattccacacatcaagctgatt 480
Db 505 AACCGAGAAACATTTATGTTGTTGGACAGAAATATTCCTTCACACATCAAGCTGATT 564
Oy 481 g 481
Db 565 g 565

RESULT 13

LOCUS BF168866 999 bp mRNA linear EST 30-OCT-2000
DEFINITION 60175335F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4016911 5',
mRNA sequence.
ACCESSION BF168866
VERSION BF168866.1 GI:11049218
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 999)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9265 row: a column: 08
High quality sequence stop: 624.
Location/Qualifiers
1. 999

FEATURES
source

/organism="Mus musculus"
/strain="C57BL/6J (f1)"
/db_xref="taxon:10090"
/clone="IMAGE:4016911"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/note="Organ: Lung; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 261 a 278 c 297 g 162 t
ORIGIN 1 others

Query Match 40.0%; Score 431.6; DB 10; Length 999;
Best Local Similarity 93.0%; Pred No. 3.2e-89;
Matches 452; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
Oy 1 atggagccattcaagcagagaagtgaggaacttattacatcgagagagagctgggg 60
Db 109 ATGAGACGCTCAACAGCAGAGAGTGGAGGACTTTATGACATCGAGAGAGAGCTGGGC 168

Oy 61 agtggcagcttgcattcgtgaaagaatgcccggagaagaagcaggggcttgatgca 120
Db 169 AGTGGCAGCTTTCCTATCGTAAGAAAGTCCGGGAGAGAGCACAGGCTGGAGTATGCA 228
Oy 121 gccaaattcaagaagcggcagagcggcgagccggcggtgtgagccggagagag 180
Db 229 GCCAAGTCAATTAAAGAGAGCAGAGAGCGGGCCAGCCGTCGGGGCGGTGTCGGGAGGAA 268
Oy 181 atcagcggagagtgagatcctcgaggcaggtgctgacacacaaatgcatcagctgac 240
Db 289 ATCGACGGGAGGTGAGCATCTGCGGAGGTCTGACCCCAACATCATCAGCTGCAC 348
Oy 241 gacgtcatgagaccgcaccgcgcgtggtgacatcctttagctagctgagtgagagag 300
Db 349 GACGCTATGAGAACCCGACCGACGCTGCTCTATCTTACCTTAGCTAGTGTCCGAGAGAA 408
Oy 301 cctctgattccttgccaggaagaagtaactgagtgaggaaggaccagcttcatt 360
Db 409 CTGTTTGATTCTCGGCCAGAGAGAGTCTTAAGTGAGAGAGAGACACACCTTCATT 468
Oy 361 aagcagaatcctgagtgagggtgaaactccttcacacaaagaagaatttcactgagtc 420
Db 469 AACGACATCTCGATGGGGGAGAACTTACCTTCACACAAAGAACTTGTCTGATCTC 528
Oy 421 aagcagaagaacatactgctgttagaagaagaatattccattccacacatcaagctgatt 480
Db 529 AACCGAGAAACATTCATGTTGTTGGACAGAAATATTCCTTCACACATCAAGCTGATT 588
Oy 481 gacttt 486
Db 589 GGAAGCTT 594

RESULT 14

LOCUS BE733365 1127 bp mRNA linear EST 15-SEP-2000
DEFINITION 601567911F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842667 5',
mRNA sequence.
ACCESSION BE733365
VERSION BE733365.1 GI:10147357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1127)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.Llnl.gov
Plate: LLM536 row: e column: 04
High quality sequence stop: 723.
Location/Qualifiers
1. 1127

FEATURES
source

/organism="Homo sapiens"
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/clone="IMAGE:3842667"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(C). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 268 a 305 c 357 g 197 t

ORIGIN

Query Match 39.8%; Score 429.8; DB 10; Length 1127;

Best Local Similarity 73.8%; Pred. No. 8.8e-85; Indels 1; Gaps 1;

Matches 559; Conservative 0; Mismatches 197;

1 atggagccattcaagcaagagtgagagcattttagacatcgagagagctggag 60
148 ATGTCCAGCTTCAGCAGAGAGAGCTGAGACCTTTATGAGATGGGAGAGAGCTGGC 207
61 agtggccagtttgccatcgtagaagaatgacggagagagcagggcttgagatgca 120
208 ACCGGCCAGTTTGCATCGTGGGAGAGTCCCGGAGAGGGGAGGAGAGAGTACGCA 267
121 gccaaattcaaaagaagcgagagccggcgagccggcggtgtgagccggagagag 180
268 GCCAAGTTTATCAAGAGAGCGCGCTGTATCATCACCGCGGTGAGCGGGAGAGG 327
181 atcgagcggagtgagagcctcctgagcagtgctgacacacatgcatcagctgac 240
328 ATCGAGCGGAGAGTGAACATCTCGCGGAGATCCGCGACCCACATCATCACCTTGAC 387
241 gacgtatagaaacacgacgagtggtgacacatcctttagctgagtagagagag 300
388 GACATCTTGAACAACAAGAGAGAGGTCCTCATCTGAGACTGTCTCTGCGGGAG 447
301 ccttcgattcctgagccagagagtgacactgagtgagagagagccacacatcatt 360
448 CTCTTGACTTCTCTGCGGAGAGAGAGTGTGACGAGAGAGAGGACCCACGATTCTTC 507
361 aagcagatcctggatgagtgagtaactccttcaacaagaataatgtctactttagtc 420
508 AAGCAATCTTGAAGAGAGAGAGGTCCTCATCTGAGACTGTCTCTGCGGGAG 567
421 aagcagaaacatagtggtgtagaagaataatcctcattccacacacacagctgatt 480
568 AAGCCGGAACATCATCTGCTGTGAGAGAGAGTGTGACGAGAGAGAGAGAGTTCATC 627
481 gacttggtcctgagcagaataagagatgagtggaatttaagaatttttggagag 540
628 GACTTGGGATCGCGCAGAGATCGAGGCGGAGAGAGTTCAGAGACATCTTGGCACCC 687
541 cggagatttggtgctcagaataatgtgaactacagagccctggtgctgagagctgacatg 600
688 CCGAGATTGTGGCCCAAGAGATTGTGAATAGAGCCGCTGGGAGAGGAGAGATG 747
601 tggagatagagcgtcatcactcactcctttaaagtggagacatcccttctctggagag 660
748 TGGAGCATCGGTGTATACCTATATCTCTGAGGTTAAATTCCTGATCTGGCCAGAA 807
661 aagaaagcagaagaacactggaataatcatcagtagagtagagactttagagagattc 720
808 CCAAGGAGAGAGAGCTCAACAAGATTCCAGCCGT-AACTAGCATTTGACACAGAGATCC 866
721 ttcaagcatatcgagcagagctgacagagacttattc 757
867 TTAGGAACCAACACTAAGTTGGCGCAGAGGTTTCATCC 903

RESULT 15

BF727181

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF727181 671 bp mRNA linear EST 05-JAN-2001
by17706.y1 Human Lens cDNA (Un-normalized, unamplified): By Homo
sapiens cDNA clone by17706 5', mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 671)
Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.
NEIBANK: EST analysis and bioinformatics for ocular genomics
Invest. Ophthalmol. Vis. Sci. 41 (2000) in press
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 17 row: h column: 06
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1..671
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/db_xref="taxon:9606"
/clone="by17706"
/clone_11b="Human Lens cDNA (Un-normalized, unamplified):
By"

/issue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pCMVSPORT2. Two human lenses
from different adults (both approximately 40 years old)
together yielded 20ug of total RNA and 150ng mRNA for cDNA
library synthesis. A directionally cloned cDNA library in
the pCMVSPORT2 vector was constructed at Life Technologies
essentially following the protocols of the Superscript
Plasmid System full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetechn.com/). First strand synthesis was
carried out using a Not I primer-adaptor
15'-pGATGTTTCTGATCGCGGAGCGGCGCC(17)15-3'. Not I/bjunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (INSC)."

BASE COUNT

159 a 197 c 201 g 113 t

ORIGIN

Query Match 39.6%; Score 428.2; DB 10; Length 671;
Best Local Similarity 77.6%; Pred. No. 1.7e-88; Indels 0; Gaps 0;

Matches 517; Conservative 0; Mismatches 149;

74 ccacgtgaaagagtgccggagagagcagggcttgagtagatgacagcaattcatca 133
6 CGATGTCGGGAAGTCCCGCAGAGAGGAGAGAGTATGACCAAGTTCATCA 65
134 aagaagcagagacccgggagccggcggtgtgagccggagagagatcgagcggagag 193
66 AGAAGCGCGCTGTATTCACACCGCGGTGAGCGGAGAGAGTTCGAGCGGAGAG 125
194 tagacatcctgagcagtgctgacacacacatgcatcagctgtagcagagcttagaga 253
126 TGAACATCTTGGGAGAGATCCGGCAACATATATACCTGCACGACATCTTGAGAA 185
254 accgcacagcagtggtgacatcctttagctagctgctgagagagagccttcgatttc 313
186 ACNAGAGGAGAGTGTGCTCATCTGAGACTGTGCTGCGGAGAGCTTTGACTTCC 245
314 tggccagaagagatgacatgagtagagagagcagcagctcatcattagacagatccgg 373
246 TGGCGGAGAGAGAGTGTGACGAGAGAGAGAGAGAGAGTTCCTCAAGATCTTG 305
374 atggagtgagacatcctcacaagaagaatgtctcattttagctcaagcagaagaaca 433
306 ACAGCTTACTACTGACCTTAAGCGCATGACACTTTGACTGTAAGCGGAGAAACA 365
434 ttatgttgtagaagaataatcccatcaccacacacacagctgtagctgtgctg 493

Db	366	TCATGCTGCTGACACAGACAGCTGCCCAACCAACAGATACAAATCAAGCTCATGACTTGCGGATCG	425
Oy	494	ctcacgaatatgaaagaatggaatgtgaatttaagaatatcttttggaaagccggaattctgtg	553
Db	426	CGCACAAAGATTCGACGCGGGGACACAGATTCAAGAAACATCTTTCGGCACCCCGGAATTTGTGG	485
Oy	554	ctccagaatatgtgaacttaacgaagcccttgggtctctgaagagcttgaacatgttgaagcatatagcg	613
Db	486	CCCCAGATTTGTGAACATATGAGCCGCTTG6CCTGGAGGCGGACATGTGAGCATGTGGTG	545
Oy	614	tcatcaacttaatactcttcttaagtbgaaatccctcttccctgggaagaacgaagcagaagaa	673
Db	546	TCATACACTATATCTCTCTCTGAGCGGTGCATATCCGTTCTCGGGCGAATCCAAACAGAGAGA	605
Oy	674	caatggaataatatcacatcgaatgagttgaacttgaatgaagaaatcttcacgcatacga	733
Db	606	CGCTACCAACATCTCAGAGCCCTGAATACGACTTCGACGAGAGGATACTTTAGCAACACCA	655
Oy	734	gcgagac	739
Db	666	GCGAGC	671

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